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SEQUENCE LISTING

<110> Adra, Chaker

<120> GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND USES THEREOF

<130> A0852.70000WO00

<140> Not yet assigned

<141> 2005-03-03

<150> 60/549,865

<151> 2004-03-03

<160> 31

<170> PatentIn version 3.3

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Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr Trp Phe Leu
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Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly Asp Leu Glu
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Pro Asp Glu Pro Ile Ser Asn His Thr Pro Cys Ile Met Lys Val Asp
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Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His Ala Ile Phe
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Gly Glu Arg Ile Leu Leu Asn Gln Ala Thr Val Lys Phe His Val Asp
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Lys Lys Asp Gly His Cys Asn Val Gln Phe Ile Asn Val Gly Glu Lys
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 atg ctg ctc act ggt ttc gtg ggc aac gca ctg gcc atg ctg ctc gtg 426
 Met Leu Leu Thr Gly Phe Val Gly Asn Ala Leu Ala Met Leu Leu Val

- 12 -

60	65	70	
tcg cgc agc tac cgg cgc cgg gag agc aag cgc aag aag tcc ttc ctg Ser Arg Ser Tyr Arg Arg Arg Glu Ser Lys Arg Lys Lys Ser Phe Leu 75 80 85			474
ctg tgc atc ggc tgg ctg gcg ctc acc gac ctg gtc ggg cag ctt ctc Leu Cys Ile Gly Trp Leu Ala Leu Thr Asp Leu Val Gly Gln Leu Leu 90 95 100 105			522
acc acc ccg gtc gtc atc gtc gtg tac ctg tcc aag cag cgt tgg gag Thr Thr Pro Val Val Ile Val Val Tyr Leu Ser Lys Gln Arg Trp Glu 110 115 120			570
cac atc gac ccg tcg ggg cgg ctc tgc acc ttt ttc ggg ctg acc atg His Ile Asp Pro Ser Gly Arg Leu Cys Thr Phe Phe Gly Leu Thr Met 125 130 135			618
act gtt ttc ggg ctc tcc tcg ttg ttc atc gcc agc gcc atg gcc gtc Thr Val Phe Gly Leu Ser Ser Leu Phe Ile Ala Ser Ala Met Ala Val 140 145 150			666
gag cgg gcg ctg gcc atc agg gcg ccg cac tgg tat gcg agc cac atg Glu Arg Ala Leu Ala Ile Arg Ala Pro His Trp Tyr Ala Ser His Met 155 160 165			714
aag acg cgt gcc acc cgc gct gtg ctg ctc ggc gtg tgg ctg gcc gtg Lys Thr Arg Ala Thr Arg Ala Val Leu Leu Gly Val Trp Leu Ala Val 170 175 180 185			762
ctc gcc ttc gcc ctg ctg ccg gtg ctg ggc gtg ggc cag tac acc gtc Leu Ala Phe Ala Leu Leu Pro Val Leu Gly Val Gly Gln Tyr Thr Val 190 195 200			810
cag tgg ccc ggg acg tgg tgc ttc atc agc acc ggg cga ggg ggc aac Gln Trp Pro Gly Thr Trp Cys Phe Ile Ser Thr Gly Arg Gly Asn 205 210 215			858
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ttt gcc ttc ctg ggg ctc ttg gcg ctg aca gtc acc ttt tcc tgc aac Phe Ala Phe Leu Gly Leu Leu Ala Leu Thr Val Thr Phe Ser Cys Asn 235 240 245			954
ctg gcc acc att aag gcc ctg gtg tcc cgc tgc cgg gcc aag gcc acg Leu Ala Thr Ile Lys Ala Leu Val Ser Arg Cys Arg Ala Lys Ala Thr 250 255 260 265			1002
gca tct cag tcc agt gcc cag tgg ggc cgc atc acg acc gag acg gcc Ala Ser Gln Ser Ser Ala Gln Trp Gly Arg Ile Thr Thr Glu Thr Ala 270 275 280			1050
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ctc ctg ata atg atg ttg aaa atg atc ttc aat cag aca tca gtt gag Leu Leu Ile Met Met Leu Lys Met Ile Phe Asn Gln Thr Ser Val Glu 300 305 310			1146

- 13 -

cac tgc aag aca cac acg gag aag cag aaa gaa tgc aac ttc ttc tta 1194
 His Cys Lys Thr His Thr Glu Lys Gln Lys Glu Cys Asn Phe Phe Leu
 315 320 325

ata gct gtt cgc ctg gct tca ctg aac cag atc ttg gat cct tgg gtt 1242
 Ile Ala Val Arg Leu Ala Ser Leu Asn Gln Ile Leu Asp Pro Trp Val
 330 335 340 345

tac ctg ctg tta aga aag atc ctt ctt cga aag ttt tgc cag atc agg 1290
 Tyr Leu Leu Leu Arg Lys Ile Leu Leu Arg Lys Phe Cys Gln Ile Arg
 350 355 360

tac cac aca aac aac tat gca tcc agc tcc acc tcc tta ccc tgc cag 1338
 Tyr His Thr Asn Asn Tyr Ala Ser Ser Ser Thr Ser Leu Pro Cys Gln
 365 370 375

tgt tcc tca acc ttg atg tgg agc gac cat ttg gaa aga taa 1380
 Cys Ser Ser Thr Leu Met Trp Ser Asp His Leu Glu Arg
 380 385 390

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- 14 -

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 Ala Arg Gly Asn Leu Thr Arg Pro Pro Gly Ser Gly Glu Asp Cys Gly
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 Ser Val Ser Val Ala Phe Pro Ile Thr Met Leu Leu Thr Gly Phe Val
 50 55 60
 Gly Asn Ala Leu Ala Met Leu Leu Val Ser Arg Ser Tyr Arg Arg Arg
 65 70 75 80
 Glu Ser Lys Arg Lys Lys Ser Phe Leu Leu Cys Ile Gly Trp Leu Ala
 85 90 95
 Leu Thr Asp Leu Val Gly Gln Leu Leu Thr Thr Pro Val Val Ile Val
 100 105 110
 Val Tyr Leu Ser Lys Gln Arg Trp Glu His Ile Asp Pro Ser Gly Arg
 115 120 125
 Leu Cys Thr Phe Phe Gly Leu Thr Met Thr Val Phe Gly Leu Ser Ser
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 Leu Phe Ile Ala Ser Ala Met Ala Val Glu Arg Ala Leu Ala Ile Arg
 145 150 155 160
 Ala Pro His Trp Tyr Ala Ser His Met Lys Thr Arg Ala Thr Arg Ala
 165 170 175
 Val Leu Leu Gly Val Trp Leu Ala Val Leu Ala Phe Ala Leu Leu Pro
 180 185 190
 Val Leu Gly Val Gly Gln Tyr Thr Val Gln Trp Pro Gly Thr Trp Cys
 195 200 205
 Phe Ile Ser Thr Gly Arg Gly Gly Asn Gly Thr Ser Ser Ser His Asn
 210 215 220
 Trp Gly Asn Leu Phe Phe Ala Ser Ala Phe Ala Phe Leu Gly Leu Leu
 225 230 235 240
 Ala Leu Thr Val Thr Phe Ser Cys Asn Leu Ala Thr Ile Lys Ala Leu
 245 250 255

- 15 -

Val Ser Arg Cys Arg Ala Lys Ala Thr Ala Ser Gln Ser Ser Ala Gln
 260 265 270

Trp Gly Arg Ile Thr Thr Glu Thr Ala Ile Gln Leu Met Gly Ile Met
 275 280 285

Cys Val Leu Ser Val Cys Trp Ser Pro Leu Leu Ile Met Met Leu Lys
 290 295 300

Met Ile Phe Asn Gln Thr Ser Val Glu His Cys Lys Thr His Thr Glu
 305 310 315 320

Lys Gln Lys Glu Cys Asn Phe Phe Leu Ile Ala Val Arg Leu Ala Ser
 325 330 335

Leu Asn Gln Ile Leu Asp Pro Trp Val Tyr Leu Leu Leu Arg Lys Ile
 340 345 350

Leu Leu Arg Lys Phe Cys Gln Ile Arg Tyr His Thr Asn Asn Tyr Ala
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Ser Asp His Leu Glu Arg
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 Leu Leu Phe Trp Gly Cys Cys Val Met His Ser Trp Glu Gly His Ile
 10 15 20

aga ccc aca cgg aaa cca aac aca aag ggt aat aac tgt aga gac agt 152
 Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly Asn Asn Cys Arg Asp Ser
 25 30 35

acc ttg tgc cca gct tat gcc acc tgc acc aat aca gtg gac agt tac 200

- 16 -

Thr	Leu	Cys	Pro	Ala	Tyr	Ala	Thr	Cys	Thr	Asn	Thr	Val	Asp	Ser	Tyr	
40						45					50					
tat	tgc	gct	tgc	aaa	caa	ggc	ttc	ctg	tcc	agc	aat	ggg	caa	aat	cac	248
Tyr	Cys	Ala	Cys	Lys	Gln	Gly	Phe	Leu	Ser	Ser	Asn	Gly	Gln	Asn	His	
55					60					65					70	
ttc	aag	gat	cca	gga	gtg	cga	tgc	aaa	gat	att	gat	gaa	tgt	tct	caa	296
Phe	Lys	Asp	Pro	Gly	Val	Arg	Cys	Lys	Asp	Ile	Asp	Glu	Cys	Ser	Gln	
				75					80						85	
agc	ccc	cag	ccc	tgt	ggc	cct	aac	tca	tcc	tgc	aaa	aac	ctg	tca	ggg	344
Ser	Pro	Gln	Pro	Cys	Gly	Pro	Asn	Ser	Ser	Cys	Lys	Asn	Leu	Ser	Gly	
			90					95					100			
agg	tac	aag	tgc	agc	tgt	tta	gat	ggc	ttc	tct	tct	ccc	act	gga	aat	392
Arg	Tyr	Lys	Cys	Ser	Cys	Leu	Asp	Gly	Phe	Ser	Ser	Pro	Thr	Gly	Asn	
		105						110					115			
gac	tgg	gtc	cca	gga	aag	ccg	ggc	aat	ttc	tcc	tgt	act	gat	atc	aat	440
Asp	Trp	Val	Pro	Gly	Lys	Pro	Gly	Asn	Phe	Ser	Cys	Thr	Asp	Ile	Asn	
	120					125					130					
gag	tgc	ctc	acc	agc	agc	gtc	tgc	cct	gag	cat	tct	gac	tgt	gtc	aac	488
Glu	Cys	Leu	Thr	Ser	Ser	Val	Cys	Pro	Glu	His	Ser	Asp	Cys	Val	Asn	
135					140					145					150	
tcc	atg	gga	agc	tac	agt	tgc	agc	tgt	caa	gtt	gga	ttc	atc	tct	aga	536
Ser	Met	Gly	Ser	Tyr	Ser	Cys	Ser	Cys	Gln	Val	Gly	Phe	Ile	Ser	Arg	
				155					160						165	
aac	tcc	acc	tgt	gaa	gac	gtg	gat	gaa	tgt	gca	gat	cca	aga	gct	tgc	584
Asn	Ser	Thr	Cys	Glu	Asp	Val	Asp	Glu	Cys	Ala	Asp	Pro	Arg	Ala	Cys	
			170					175					180			
cca	gag	cat	gca	act	tgt	aat	aac	act	gtt	gga	aac	tac	tct	tgt	ttc	632
Pro	Glu	His	Ala	Thr	Cys	Asn	Asn	Thr	Val	Gly	Asn	Tyr	Ser	Cys	Phe	
		185					190					195				
tgc	aac	cca	gga	ttt	gaa	tcc	agc	agt	ggc	cac	ttg	agt	ttc	cag	ggc	680
Cys	Asn	Pro	Gly	Phe	Glu	Ser	Ser	Ser	Gly	His	Leu	Ser	Phe	Gln	Gly	
	200					205					210					
ctc	aaa	gca	tgc	tgt	gaa	gat	att	gat	gaa	tgc	act	gaa	atg	tgc	ccc	728
Leu	Lys	Ala	Ser	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Thr	Glu	Met	Cys	Pro	
215					220					225					230	
atc	aat	tca	aca	tgc	acc	aac	act	cct	ggg	agc	tac	ttt	tgc	acc	tgc	776
Ile	Asn	Ser	Thr	Cys	Thr	Asn	Thr	Pro	Gly	Ser	Tyr	Phe	Cys	Thr	Cys	
				235					240					245		
cac	cct	ggc	ttt	gca	cca	agc	aat	gga	cag	ttg	aat	ttc	aca	gac	caa	824
His	Pro	Gly	Phe	Ala	Pro	Ser	Asn	Gly	Gln	Leu	Asn	Phe	Thr	Asp	Gln	
			250					255					260			
gga	gtg	gaa	tgt	aga	gat	att	gat	gag	tgc	cgc	caa	gat	cca	tca	acc	872
Gly	Val	Glu	Cys	Arg	Asp	Ile	Asp	Glu	Cys	Arg	Gln	Asp	Pro	Ser	Thr	
		265					270					275				
tgt	ggc	cct	aat	tct	atc	tgc	acc	aat	gcc	ctg	ggc	tcc	tac	agc	tgt	920
Cys	Gly	Pro	Asn	Ser	Ile	Cys	Thr	Asn	Ala	Leu	Gly	Ser	Tyr	Ser	Cys	
	280					285					290					

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ggc tgc att gca ggc ttt cat ccc aat cca gaa ggc tcc cag aaa gat	968
Gly Cys Ile Ala Gly Phe His Pro Asn Pro Glu Gly Ser Gln Lys Asp	
295 300 305 310	
ggc aac ttc agc tgc caa agg gtt ctc ttc aaa tgt aag gaa gat gtg	1016
Gly Asn Phe Ser Cys Gln Arg Val Leu Phe Lys Cys Lys Glu Asp Val	
315 320 325	
ata ccc gat aat aag cag atc cag caa tgc caa gag gga acc gca gtg	1064
Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys Gln Glu Gly Thr Ala Val	
330 335 340	
aaa cct gca tat gtc tcc ttt tgt gca caa ata aat aac atc ttc agc	1112
Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln Ile Asn Asn Ile Phe Ser	
345 350 355	
gtt ctg gac aaa gtg tgt gaa aat aaa acg acc gta gtt tct ctg aag	1160
Val Leu Asp Lys Val Cys Glu Asn Lys Thr Thr Val Val Ser Leu Lys	
360 365 370	
aat aca act gag agc ttt gtc cct gtg ctt aaa caa ata tcc acg tgg	1208
Asn Thr Thr Glu Ser Phe Val Pro Val Leu Lys Gln Ile Ser Thr Trp	
375 380 385 390	
act aaa ttc acc aag gaa gag acg tcc tcc ctg gcc aca gtc ttc ctg	1256
Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser Leu Ala Thr Val Phe Leu	
395 400 405	
gag agt gtg gaa agc atg aca ctg gca tct ttt tgg aaa ccc tca gca	1304
Glu Ser Val Glu Ser Met Thr Leu Ala Ser Phe Trp Lys Pro Ser Ala	
410 415 420	
aat atc act ccg gct gtt cgg acg gaa tac tta gac att gag agc aaa	1352
Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr Leu Asp Ile Glu Ser Lys	
425 430 435	
gtt atc aac aaa gaa tgc agt gaa gag aat gtg acg ttg gac ttg gta	1400
Val Ile Asn Lys Glu Cys Ser Glu Glu Asn Val Thr Leu Asp Leu Val	
440 445 450	
gcc aag ggg gat aag atg aag atc ggg tgt tcc aca att gag gaa tct	1448
Ala Lys Gly Asp Lys Met Lys Ile Gly Cys Ser Thr Ile Glu Glu Ser	
455 460 465 470	
gaa tcc aca gag acc act ggt gtg gct ttt gtc tcc ttt gtg ggc atg	1496
Glu Ser Thr Glu Thr Thr Gly Val Ala Phe Val Ser Phe Val Gly Met	
475 480 485	
gaa tcg gtt tta aat gag cgc ttc ttc aaa gac cac cag gct ccc ttg	1544
Glu Ser Val Leu Asn Glu Arg Phe Phe Lys Asp His Gln Ala Pro Leu	
490 495 500	
acc acc tct gag atc aag ctg aag atg aat tct cga gtc gtt ggg ggc	1592
Thr Thr Ser Glu Ile Lys Leu Lys Met Asn Ser Arg Val Val Gly Gly	
505 510 515	
ata atg act gga gag aag aaa gac ggc ttc tca gat cca atc atc tac	1640
Ile Met Thr Gly Glu Lys Lys Asp Gly Phe Ser Asp Pro Ile Ile Tyr	
520 525 530	
act ctg gag aac att cag cca aag cag aag ttt gag agg ccc atc tgt	1688

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Thr	Leu	Glu	Asn	Ile	Gln	Pro	Lys	Gln	Lys	Phe	Glu	Arg	Pro	Ile	Cys		
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Val	Ser	Trp	Ser	Thr	Asp	Val	Lys	Gly	Gly	Arg	Trp	Thr	Ser	Phe	Gly		
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tgt	gtg	atc	ctg	gaa	gct	tct	gag	aca	tat	acc	atc	tgc	agc	tgt	aat	1784	
Cys	Val	Ile	Leu	Glu	Ala	Ser	Glu	Thr	Tyr	Thr	Ile	Cys	Ser	Cys	Asn		
			570					575					580				
cag	atg	gca	aat	ctt	gcc	ggt	atc	atg	gcg	tct	ggg	gag	ctc	acg	atg	1832	
Gln	Met	Ala	Asn	Leu	Ala	Val	Ile	Met	Ala	Ser	Gly	Glu	Leu	Thr	Met		
		585					590					595					
gac	ttt	tcc	ttg	tac	atc	att	agc	cat	gta	ggc	att	atc	atc	tcc	ttg	1880	
Asp	Phe	Ser	Leu	Tyr	Ile	Ile	Ser	His	Val	Gly	Ile	Ile	Ile	Ser	Leu		
	600					605					610						
gtg	tgc	ctc	gtc	ttg	gcc	atc	gcc	acc	ttt	ctg	ctg	tgt	cgc	tcc	atc	1928	
Val	Cys	Leu	Val	Leu	Ala	Ile	Ala	Thr	Phe	Leu	Leu	Cys	Arg	Ser	Ile		
	615				620					625					630		
cga	aat	cac	aac	acc	tac	ctc	cac	ctg	cac	ctc	tgc	gtg	tgt	ctc	ctc	1976	
Arg	Asn	His	Asn	Thr	Tyr	Leu	His	Leu	His	Leu	Cys	Val	Cys	Leu	Leu		
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Leu	Ala	Lys	Thr	Leu	Phe	Leu	Ala	Gly	Ile	His	Lys	Thr	Asp	Asn	Lys		
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Met	Gly	Cys	Ala	Ile	Ile	Ala	Gly	Phe	Leu	His	Tyr	Leu	Phe	Leu	Ala		
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tgc	ttc	ttc	tgg	atg	ctg	gtg	gag	gct	gtg	ata	ctg	ttc	ttg	atg	gtc	2120	
Cys	Phe	Phe	Trp	Met	Leu	Val	Glu	Ala	Val	Ile	Leu	Phe	Leu	Met	Val		
	680					685					690						
aga	aac	ctg	aag	gtg	gtg	aat	tac	ttc	agc	tct	cgc	aac	atc	aag	atg	2168	
Arg	Asn	Leu	Lys	Val	Val	Asn	Tyr	Phe	Ser	Ser	Arg	Asn	Ile	Lys	Met		
	695				700					705				710			
ctg	cac	atc	tgt	gcc	ttt	ggg	tat	ggg	ctg	ccg	atg	ctg	gtg	gtg	gtg	2216	
Leu	His	Ile	Cys	Ala	Phe	Gly	Tyr	Gly	Leu	Pro	Met	Leu	Val	Val	Val		
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Ile	Ser	Ala	Ser	Val	Gln	Pro	Gln	Gly	Tyr	Gly	Met	His	Asn	Arg	Cys		
			730					735					740				
tgg	ctg	aat	aca	gag	aca	ggg	ttc	atc	tgg	agt	ttc	ttg	ggg	cca	gtt	2312	
Trp	Leu	Asn	Thr	Glu	Thr	Gly	Phe	Ile	Trp	Ser	Phe	Leu	Gly	Pro	Val		
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tgc	aca	gtt	ata	gtg	atc	aac	tcc	ctt	ctc	ctg	acc	tgg	acc	ttg	tgg	2360	
Cys	Thr	Val	Ile	Val	Ile	Asn	Ser	Leu	Leu	Leu	Thr	Trp	Thr	Leu	Trp		
		760				765					770						
atc	ctg	agg	cag	agg	ctt	tcc	agt	gtt	aat	gcc	gaa	gtc	tca	acg	cta	2408	
Ile	Leu	Arg	Gln	Arg	Leu	Ser	Ser	Val	Asn	Ala	Glu	Val	Ser	Thr	Leu		
	775				780					785					790		

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aaa gac acc agg tta ctg acc ttc aag gcc ttt gcc cag ctc ttc atc      2456
Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Phe Ala Gln Leu Phe Ile
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ctg ggc tgc tcc tgg gtg ctg ggc att ttt cag att gga cct gtg gca      2504
Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly Pro Val Ala
              810                      815                      820

ggg gtc atg gct tac ctg ttc acc atc atc aac agc ctg cag ggg gcc      2552
Gly Val Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu Gln Gly Ala
              825                      830                      835

ttc atc ttc ctc atc cac tgt ctg ctc aac ggc cag gta cga gaa gaa      2600
Phe Ile Phe Leu Ile His Cys Leu Leu Asn Gly Gln Val Arg Glu Glu
              840                      845                      850

tac aag agg tgg atc act ggg aag acg aag ccc agc tcc cag tcc cag      2648
Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys Pro Ser Ser Gln Ser Gln
855                      860                      865                      870

acc tca agg atc ttg ctg tcc tcc atg cca tcc gct tcc aag acg ggt      2696
Thr Ser Arg Ile Leu Leu Ser Ser Met Pro Ser Ala Ser Lys Thr Gly
              875                      880                      885

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20              25                      30

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Asn Asn Cys Arg Asp Ser Thr Leu Cys Pro Ala Tyr Ala Thr Cys Thr
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Asn Thr Val Asp Ser Tyr Tyr Cys Ala Cys Lys Gln Gly Phe Leu Ser

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- 20 -

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Ser Asn Gly Gln Asn His Phe Lys Asp Pro Gly Val Arg Cys Lys Asp				
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Ile Asp Glu Cys Ser Gln Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser				
	85		90	95
Cys Lys Asn Leu Ser Gly Arg Tyr Lys Cys Ser Cys Leu Asp Gly Phe				
	100		105	110
Ser Ser Pro Thr Gly Asn Asp Trp Val Pro Gly Lys Pro Gly Asn Phe				
	115		120	125
Ser Cys Thr Asp Ile Asn Glu Cys Leu Thr Ser Ser Val Cys Pro Glu				
	130		135	140
His Ser Asp Cys Val Asn Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln				
	145		150	155 160
Val Gly Phe Ile Ser Arg Asn Ser Thr Cys Glu Asp Val Asp Glu Cys				
	165		170	175
Ala Asp Pro Arg Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val				
	180		185	190
Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly				
	195		200	205
His Leu Ser Phe Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu				
	210		215	220
Cys Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly				
	225		230	235 240
Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Asn Gly Gln				
	245		250	255
Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys				
	260		265	270
Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala				
	275		280	285
Leu Gly Ser Tyr Ser Cys Gly Cys Ile Ala Gly Phe His Pro Asn Pro				
	290		295	300

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Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe
 305 310 315 320

Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys
 325 330 335

Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln
 340 345 350

Ile Asn Asn Ile Phe Ser Val Leu Asp Lys Val Cys Glu Asn Lys Thr
 355 360 365

Thr Val Val Ser Leu Lys Asn Thr Thr Glu Ser Phe Val Pro Val Leu
 370 375 380

Lys Gln Ile Ser Thr Trp Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser
 385 390 395 400

Leu Ala Thr Val Phe Leu Glu Ser Val Glu Ser Met Thr Leu Ala Ser
 405 410 415

Phe Trp Lys Pro Ser Ala Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr
 420 425 430

Leu Asp Ile Glu Ser Lys Val Ile Asn Lys Glu Cys Ser Glu Glu Asn
 435 440 445

Val Thr Leu Asp Leu Val Ala Lys Gly Asp Lys Met Lys Ile Gly Cys
 450 455 460

Ser Thr Ile Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe
 465 470 475 480

Val Ser Phe Val Gly Met Glu Ser Val Leu Asn Glu Arg Phe Phe Lys
 485 490 495

Asp His Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn
 500 505 510

Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe
 515 520 525

Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Ile Gln Pro Lys Gln Lys
 530 535 540

Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly

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545		550		555		560
Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr	565	570	575			
Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala	580	585	590			
Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val	595	600	605			
Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe	610	615	620			
Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His	625	630	635			640
Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile	645	650	655			
His Lys Thr Asp Asn Lys Met Gly Cys Ala Ile Ile Ala Gly Phe Leu	660	665	670			
His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val	675	680	685			
Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser	690	695	700			
Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu	705	710	715			720
Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr	725	730	735			
Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp	740	745	750			
Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu	755	760	765			
Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn	770	775	780			
Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala	785	790	795			800

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Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe
 805 810 815

Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile
 820 825 830

Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn
 835 840 845

Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys
 850 855 860

Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro
 865 870 875 880

Ser Ala Ser Lys Thr Gly
 885

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (213)..(1229)

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 agatgaaggc ctagacgcag gatctttaat gaaaaaacac ttggggccact tcaagacgac 120
 aaacgctcac tgggcaaaac accttcaactg aaaagagacc tcatattatg caaaaaaaat 180
 cttaaaaggc ctctgccttc agaagttaca ag atg atc aat tca acc tcc aca 233
 Met Ile Asn Ser Thr Ser Thr
 1 5
 cag cct cca gat gaa tcc tgc tct cag aac ctc ctg atc act cag cag 281
 Gln Pro Pro Asp Glu Ser Cys Ser Gln Asn Leu Leu Ile Thr Gln Gln
 10 15 20
 atc att cct gtg ctg tac tgt atg gtc ttc att gca gga atc cta ctc 329
 Ile Ile Pro Val Leu Tyr Cys Met Val Phe Ile Ala Gly Ile Leu Leu
 25 30 35
 aat gga gtg tca gga tgg ata ttc ttt tac gtg ccc agc tct gag agt 377
 Asn Gly Val Ser Gly Trp Ile Phe Phe Tyr Val Pro Ser Ser Glu Ser
 40 45 50 55
 ttc atc atc tat ctc aag aac att gtt att gct gac ttt gtg atg agc 425
 Phe Ile Ile Tyr Leu Lys Asn Ile Val Ile Ala Asp Phe Val Met Ser
 60 65 70

- 24 -

ctg act ttt cct ttc aag atc ctt ggt gac tca ggc ctt ggt ccc tgg	473
Leu Thr Phe Pro Phe Lys Ile Leu Gly Asp Ser Gly Leu Gly Pro Trp	
75 80 85	
cag ctg aac gtg ttt gtg tgc agg gtc tct gcc gtg ctc ttc tac gtc	521
Gln Leu Asn Val Phe Val Cys Arg Val Ser Ala Val Leu Phe Tyr Val	
90 95 100	
aac atg tac gtc agc att gtg ttc ttt ggg ctc atc agc ttt gac aga	569
Asn Met Tyr Val Ser Ile Val Phe Phe Gly Leu Ile Ser Phe Asp Arg	
105 110 115	
tat tat aaa att gta aag cct ctt tgg act tct ttc atc cag tca gtg	617
Tyr Tyr Lys Ile Val Lys Pro Leu Trp Thr Ser Phe Ile Gln Ser Val	
120 125 130 135	
agt tac agc aaa ctt ctg tca gtg ata gta tgg atg ctc atg ctc ctc	665
Ser Tyr Ser Lys Leu Leu Ser Val Ile Val Trp Met Leu Met Leu Leu	
140 145 150	
ctt gct gtt cca aat att att ctc acc aac cag agt gtt agg gag gtt	713
Leu Ala Val Pro Asn Ile Ile Leu Thr Asn Gln Ser Val Arg Glu Val	
155 160 165	
aca caa ata aaa tgt ata gaa ctg aaa agt gaa ctg gga cgg aag tgg	761
Thr Gln Ile Lys Cys Ile Glu Leu Lys Ser Glu Leu Gly Arg Lys Trp	
170 175 180	
cac aaa gca tca aac tac atc ttc gtg gcc atc ttc tgg att gtg ttt	809
His Lys Ala Ser Asn Tyr Ile Phe Val Ala Ile Phe Trp Ile Val Phe	
185 190 195	
ctt ttg tta atc gtt ttc tat act gct atc aca aag aaa atc ttt aag	857
Leu Leu Leu Ile Val Phe Tyr Thr Ala Ile Thr Lys Lys Ile Phe Lys	
200 205 210 215	
tcc cac ctt aag tca agt cgg aat tcc act tcg gtc aaa aag aaa tct	905
Ser His Leu Lys Ser Ser Arg Asn Ser Thr Ser Val Lys Lys Lys Ser	
220 225 230	
agc cgc aac ata ttc agc atc gtg ttt gtg ttt ttt gtc tgt ttt gta	953
Ser Arg Asn Ile Phe Ser Ile Val Phe Val Phe Phe Val Cys Phe Val	
235 240 245	
cct tac cat att gcc aga atc ccc tac aca aag agt cag acc gaa gct	1001
Pro Tyr His Ile Ala Arg Ile Pro Tyr Thr Lys Ser Gln Thr Glu Ala	
250 255 260	
cat tac agc tgc cag tca aaa gaa atc ttg cgg tat atg aaa gaa ttc	1049
His Tyr Ser Cys Gln Ser Lys Glu Ile Leu Arg Tyr Met Lys Glu Phe	
265 270 275	
act ctg cta cta tct gct gca aat gta tgc ttg gac cct att att tat	1097
Thr Leu Leu Leu Ser Ala Ala Asn Val Cys Leu Asp Pro Ile Ile Tyr	
280 285 290 295	
ttc ttt cta tgc cag ccg ttt agg gaa atc tta tgt aag aaa ttg cac	1145
Phe Phe Leu Cys Gln Pro Phe Arg Glu Ile Leu Cys Lys Lys Leu His	
300 305 310	
att cca tta aaa gct cag aat gac cta gac att tcc aga atc aaa aga	1193
Ile Pro Leu Lys Ala Gln Asn Asp Leu Asp Ile Ser Arg Ile Lys Arg	

- 25 -

315	320	325	
gga aat aca aca ctt gaa agc aca gat act ttg tga gttcctaccc			1239
Gly Asn Thr Thr Leu Glu Ser Thr Asp Thr Leu			
330	335		
tcttccaaag aaagaccacg tgtgcatggt gtcattcttca attacataac agaaatcaat			1299
aagatatgtg ccctcatcat aaatatcatc tctagcactg ccatccaatt tagttcaata			1359
aaattcaaat ataagtttcc atgctttttt gtaacatcaa agaaaacata cccatcagta			1419
attttctctaa tactgacctt tctattctct attaataaaa aattaataca tacaattatt			1479
caattctatt atattaaaat aagttaaagt ttataaccac tagtctgggtc agttaatgta			1539
gaaattttaa tagtaaataa aacacaacat aatcaaagac aactcactca ggcattcttct			1599
ttctctaaat accagaatct agtatgtaat tgttttcaac actgtcctta aagactaact			1659
tgaaagcagg cacagtttga tgaagggcta gagagctggt tgcaataaaa agtcagggtt			1719
ttttcctgat ttgaagaagc aggaaaagct gacacccaga caatcactta agaaacccct			1779
tattgatgta tttcatggca ctgcaaagga agaggaatat taattgtata cttagcaaga			1839
aaattttttt tttctgatag cactttgagg atattagata catgctaaat atgttttcta			1899
caaagactta cgtcatttaa tgagcctggg gttctgggtgt tagaatattt ttaagtaggc			1959
tttactgaga gaaactaaat attggcatac gttatcagca acttcccctg ttcaatagta			2019
tgggaaaaat aagatgactg ggaaaaagac acaccacac cgtagaacat atattaatct			2079
actggcgaat gggaaaggag accattttct tagaaagcaa ataaacttga tttttttaa			2139
tctaaaattt acattaatga gtgcaaaata acacataaaa tgaaaattca cacatcacat			2199
ttttctggaa aacagacgga ttttacttct ggagacatgg catacgggtta ctgacttatg			2259
agctaccaa actaaattct ttctctgcta ttaactggct agaagacatt catctatttt			2319
tcaaagtgtc tttcaaaaca tttttataag taatgtttgt atctatttca tgctttactg			2379
tctatatact aataaagaaa tgttttaata ccgaaaaaaaa aaaaaaaaaa			2428

<210> 11
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 11

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1				5				10						15	

Asn	Leu	Leu	Ile	Thr	Gln	Gln	Ile	Ile	Pro	Val	Leu	Tyr	Cys	Met	Val
	20						25						30		

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Phe Ile Ala Gly Ile Leu Leu Asn Gly Val Ser Gly Trp Ile Phe Phe
 35 40 45

Tyr Val Pro Ser Ser Glu Ser Phe Ile Ile Tyr Leu Lys Asn Ile Val
 50 55 60

Ile Ala Asp Phe Val Met Ser Leu Thr Phe Pro Phe Lys Ile Leu Gly
 65 70 75 80

Asp Ser Gly Leu Gly Pro Trp Gln Leu Asn Val Phe Val Cys Arg Val
 85 90 95

Ser Ala Val Leu Phe Tyr Val Asn Met Tyr Val Ser Ile Val Phe Phe
 100 105 110

Gly Leu Ile Ser Phe Asp Arg Tyr Tyr Lys Ile Val Lys Pro Leu Trp
 115 120 125

Thr Ser Phe Ile Gln Ser Val Ser Tyr Ser Lys Leu Leu Ser Val Ile
 130 135 140

Val Trp Met Leu Met Leu Leu Leu Ala Val Pro Asn Ile Ile Leu Thr
 145 150 155 160

Asn Gln Ser Val Arg Glu Val Thr Gln Ile Lys Cys Ile Glu Leu Lys
 165 170 175

Ser Glu Leu Gly Arg Lys Trp His Lys Ala Ser Asn Tyr Ile Phe Val
 180 185 190

Ala Ile Phe Trp Ile Val Phe Leu Leu Leu Ile Val Phe Tyr Thr Ala
 195 200 205

Ile Thr Lys Lys Ile Phe Lys Ser His Leu Lys Ser Ser Arg Asn Ser
 210 215 220

Thr Ser Val Lys Lys Lys Ser Ser Arg Asn Ile Phe Ser Ile Val Phe
 225 230 235 240

Val Phe Phe Val Cys Phe Val Pro Tyr His Ile Ala Arg Ile Pro Tyr
 245 250 255

Thr Lys Ser Gln Thr Glu Ala His Tyr Ser Cys Gln Ser Lys Glu Ile
 260 265 270

Leu Arg Tyr Met Lys Glu Phe Thr Leu Leu Leu Ser Ala Ala Asn Val
 275 280 285

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Cys Leu Asp Pro Ile Ile Tyr Phe Phe Leu Cys Gln Pro Phe Arg Glu
 290 295 300

Ile Leu Cys Lys Lys Leu His Ile Pro Leu Lys Ala Gln Asn Asp Leu
 305 310 315 320

Asp Ile Ser Arg Ile Lys Arg Gly Asn Thr Thr Leu Glu Ser Thr Asp
 325 330 335

Thr Leu

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 <211> 1734
 <212> DNA
 <213> Homo sapiens

<220>
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 tctgcggcgt gactggaggc ccag atg gtc atc atg ggc cag tgc tac tac 111
 Met Val Ile Met Gly Gln Cys Tyr Tyr
 1 5
 aac gag acc atc ggc ttc ttc tat aac aac agt ggc aaa gag ctc agc 159
 Asn Glu Thr Ile Gly Phe Phe Tyr Asn Asn Ser Gly Lys Glu Leu Ser
 10 15 20 25
 tcc cac tgg cgg ccc aag gat gtg gtc gtg gtg gca ctg ggg ctg acc 207
 Ser His Trp Arg Pro Lys Asp Val Val Val Val Ala Leu Gly Leu Thr
 30 35 40
 gtc agc gtg ctg gtg ctg ctg acc aat ctg ctg gtc ata gca gcc atc 255
 Val Ser Val Leu Val Leu Leu Thr Asn Leu Leu Val Ile Ala Ala Ile
 45 50 55
 gcc tcc aac cgc cgc ttc cac cag ccc atc tac tac ctg ctc ggc aat 303
 Ala Ser Asn Arg Arg Phe His Gln Pro Ile Tyr Tyr Leu Leu Gly Asn
 60 65 70
 ctg gcc gcg gct gac ctc ttc gcg ggc gtg gcc tac ctc ttc ctc atg 351
 Leu Ala Ala Ala Asp Leu Phe Ala Gly Val Ala Tyr Leu Phe Leu Met
 75 80 85
 ttc cac act ggt ccc cgc aca gcc cga ctt tca ctt gag ggc tgg ttc 399
 Phe His Thr Gly Pro Arg Thr Ala Arg Leu Ser Leu Glu Gly Trp Phe
 90 95 100 105
 ctg cgg cag ggc ttg ctg gac aca agc ctc act gcg tcg gtg gcc aca 447
 Leu Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Val Ala Thr
 110 115 120

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ctg ctg gcc atc gcc gtg gag cgg cac cgc agt gtg atg gcc gtg cag	495
Leu Leu Ala Ile Ala Val Glu Arg His Arg Ser Val Met Ala Val Gln	
125 130 135	
ctg cac agc cgc ctg ccc cgt ggc cgc gtg gtc atg ctc att gtg ggc	543
Leu His Ser Arg Leu Pro Arg Gly Arg Val Val Met Leu Ile Val Gly	
140 145 150	
gtg tgg gtg gct gcc ctg ggc ctg ggg ctg ctg cct gcc cac tcc tgg	591
Val Trp Val Ala Ala Leu Gly Leu Gly Leu Leu Pro Ala His Ser Trp	
155 160 165	
cac tgc ctc tgt gcc ctg gac cgc tgc tca cgc atg gca ccc ctg ctc	639
His Cys Leu Cys Ala Leu Asp Arg Cys Ser Arg Met Ala Pro Leu Leu	
170 175 180 185	
agc cgc tcc tat ttg gcc gtc tgg gct ctg tcg agc ctg ctt gtc ttc	687
Ser Arg Ser Tyr Leu Ala Val Trp Ala Leu Ser Ser Leu Leu Val Phe	
190 195 200	
ctg ctc atg gtg gct gtg tac acc cgc att ttc ttc tac gtg cgg cgg	735
Leu Leu Met Val Ala Val Tyr Thr Arg Ile Phe Phe Tyr Val Arg Arg	
205 210 215	
cga gtg cag cgc atg gca gag cat gtc agc tgc cac ccc cgc tac cga	783
Arg Val Gln Arg Met Ala Glu His Val Ser Cys His Pro Arg Tyr Arg	
220 225 230	
gag acc acg ctc agc ctg gtc aag act gtt gtc atc atc ctg ggg gcg	831
Glu Thr Thr Leu Ser Leu Val Lys Thr Val Val Ile Ile Leu Gly Ala	
235 240 245	
ttc gtg gtc tgc tgg aca cca ggc cag gtg gta ctg ctc ctg gat ggt	879
Phe Val Val Cys Trp Thr Pro Gly Gln Val Val Leu Leu Leu Asp Gly	
250 255 260 265	
tta ggc tgt gag tcc tgc aat gtc ctg gct gta gaa aag tac ttc cta	927
Leu Gly Cys Glu Ser Cys Asn Val Leu Ala Val Glu Lys Tyr Phe Leu	
270 275 280	
ctg ttg gcc gag gcc aac tca ctg gtc aat gct gct gtg tac tct tgc	975
Leu Leu Ala Glu Ala Asn Ser Leu Val Asn Ala Ala Val Tyr Ser Cys	
285 290 295	
cga gat gct gag atg cgc cgc acc ttc cgc cgc ctt ctc tgc tgc gcg	1023
Arg Asp Ala Glu Met Arg Arg Thr Phe Arg Arg Leu Leu Cys Cys Ala	
300 305 310	
tgc ctc cgc cag tcc acc cgc gag tct gtc cac tat aca tcc tct gcc	1071
Cys Leu Arg Gln Ser Thr Arg Glu Ser Val His Tyr Thr Ser Ser Ala	
315 320 325	
cag gga ggt gcc agc act cgc atc atg ctt ccc gag aac ggc cac cca	1119
Gln Gly Gly Ala Ser Thr Arg Ile Met Leu Pro Glu Asn Gly His Pro	
330 335 340 345	
ctg atg act cca ccc ttt agc tac ctt gaa ctt cag cgg tac gcg gca	1167
Leu Met Thr Pro Pro Phe Ser Tyr Leu Glu Leu Gln Arg Tyr Ala Ala	
350 355 360	
agc aac aaa tcc aca gcc cct gat gac ttg tgg gtg ctc ctg gct caa	1215

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Ser Asn Lys Ser Thr Ala Pro Asp Asp Leu Trp Val Leu Leu Ala Gln
 365 370 375
 ccc aac caa cag gac tga ctgactggca ggacaaggtc tggcatggca 1263
 Pro Asn Gln Gln Asp
 380
 cagcaccact gccaggcctc cccaggcaca ccactctgcc cagggaatgg gggctttggg 1323
 tcactctcca ctgcctgggg gagtcagatg ggggtgcagga atctggctct tcagccatct 1383
 caggtttagg gggtttgtaa cagacattat tctgttttca ctgcgtatcc ttggttaagcc 1443
 ctgtggactg gttcctgctg tgtgatgctg agggtttttaa ggtggggaga gataagggct 1503
 ctctcggggc atgctacccg gtatgactgg gtaatgagga cagactgtgg acaccccatc 1563
 tacctgagtc tgattcttta gcagcagaga ctgaggggtg cagagtgtga gctgggaaag 1623
 gtttgtggct ccttgacagc tccagggact ggctgtccc caatagaatt gaagcagtcc 1683
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 <211> 382
 <212> PRT
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 Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
 35 40 45
 Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
 50 55 60
 Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
 65 70 75 80
 Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
 85 90 95
 Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
 100 105 110
 Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
 115 120 125

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Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
 130 135 140

Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
 145 150 155 160

Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
 165 170 175

Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
 180 185 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
 195 200 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
 210 215 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
 225 230 235 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
 245 250 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
 260 265 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
 275 280 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
 290 295 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
 305 310 315 320

Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
 325 330 335

Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
 340 345 350

Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
 355 360 365

Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp

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370 375 380

<210> 14
 <211> 993
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (993)

<400> 14

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Met Leu Pro Asp Trp Lys Ser Ser Leu Ile Leu Met Ala Tyr Ile Ile	
1 5 10 15	
atc ttc ctc act ggc ctc cct gcc aac ctc ctg gcc ctg cgg gcc ttt	96
Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe	
20 25 30	
gtg ggg cgg atc cgc cag ccc cag cct gca cct gtg cac atc ctc ctg	144
Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu	
35 40 45	
ctg agc ctg acg ctg gcc gac ctc ctc ctg ctg ctg ctg ccc ttc	192
Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Pro Phe	
50 55 60	
aag atc atc gag gct gcg tcg aac ttc cgc tgg tac ctg ccc aag gtc	240
Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val	
65 70 75 80	
gtc tgc gcc ctc acg agt ttt ggc ttc tac agc agc atc tac tgc agc	288
Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser	
85 90 95	
acg tgg ctc ctg gcg ggc atc agc atc gag cgc tac ctg gga gtg gct	336
Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala	
100 105 110	
ttc ccc gtg cag tac aag ctc tcc cgc cgg cct ctg tat gga gtg att	384
Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile	
115 120 125	
gca gct ctg gtg gcc tgg gtt atg tcc ttt ggt cac tgc acc atc gtg	432
Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val	
130 135 140	
atc atc gtt caa tac ttg aac acg act gag cag gtc aga agt ggc aat	480
Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn	
145 150 155 160	
gaa att acc tgc tac gag aac ttc acc gat aac cag ttg gac gtg gtg	528
Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val	
165 170 175	
ctg ccc gtg cgg ctg gag ctg tgc ctg gtg ctc ttc ttc atc ccc atg	576
Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met	
180 185 190	

gca Ala	gtc Val	acc Thr	atc Ile	ttc Phe	tgc Cys	tac Tyr	tgg Trp	cgt Arg	ttt Phe	gtg Val	tgg Trp	atc Ile	atg Met	ctc Leu	tcc Ser	624
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cag Gln	ccc Pro	ctt Leu	gtg Val	ggg Gly	gcc Ala	cag Gln	agg Arg	cgg Arg	cgc Arg	cga Arg	gcc Ala	gtg Val	ggg Gly	ctg Leu	gct Ala	672
210215220																
gtg Val	gtg Val	acg Thr	ctg Leu	ctc Leu	aat Asn	ttc Phe	ctg Leu	gtg Val	tgc Cys	ttc Phe	gga Gly	cct Pro	tac Tyr	aac Asn	gtg Val	720
225230235240																
tcc Ser	cac His	ctg Leu	gtg Val	ggg Gly	tat Tyr	cac His	cag Gln	aga Arg	aaa Lys	agc Ser	ccc Pro	tgg Trp	tgg Trp	cgg Arg	tca Ser	768
245250255																
ata Ile	gcc Ala	gtg Val	gtg Val	ttc Phe	agt Ser	tca Ser	ctc Leu	aac Asn	gcc Ala	agt Ser	ctg Leu	gac Asp	ccc Pro	ctg Leu	ctc Leu	816
260265270																
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275280285																
cag Gln	gtg Val	ctg Leu	cgg Arg	aat Asn	cag Gln	ggc Gly	tcc Ser	tcc Ser	ctg Leu	ttg Leu	gga Gly	cgc Arg	aga Arg	ggc Gly	aaa Lys	912
290295300																
gac Asp	aca Thr	gca Ala	gag Glu	ggg Gly	aca Thr	aat Asn	gag Glu	gac Asp	agg Arg	ggt Gly	gtg Val	ggt Gly	caa Gln	gga Gly	gaa Glu	960
305310315320																
ggg Gly	atg Met	cca Pro	agt Ser	tcg Ser	gac Asp	ttc Phe	act Thr	aca Thr	gag Glu	tag						993
325330																

<400> 15

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- 34 -

Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
 325 330

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 <212> DNA
 <213> Homo sapiens

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 <222> (72)..(1085)

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 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr
 1 5 10
 agc gac ctc tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg 158
 Ser Asp Leu Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu
 15 20 25
 gcc atc gac ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc 206
 Ala Ile Asp Pro Leu Arg Val Ala Pro Leu Tyr Ala Ala Ile
 30 35 40 45
 ttc ctg gtg ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg 254
 Phe Leu Val Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly
 50 55 60
 aag gtg gcc cgc cgg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc 302
 Lys Val Ala Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala
 65 70 75
 gtg gcg gat ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc 350
 Val Ala Asp Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro
 80 85 90
 att gcc cgt gga ggc cac tgg ccg tat ggt gca gtg ggc tgt cgg gcg 398
 Ile Ala Arg Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala
 95 100 105
 ctg ccc tcc atc atc ctg ctg acc atg tat gcc agc gtc ctg ctc ctg 446
 Leu Pro Ser Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu
 110 115 120 125
 gca gct ctc agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg 494
 Ala Ala Leu Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp
 130 135 140
 tgg tct acg gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca 542
 Trp Ser Thr Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala
 145 150 155
 gcc tgg aca ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cgc 590
 Ala Trp Thr Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg
 160 165 170
 cgg ctg cac cag gag cac ttc cca gcc cgg ctg cag tgt gtg gtg gac 638

- 35 -

Arg Leu His Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp
 175 180 185
 tac ggc ggc tcc tcc agc acc gag aat gcg gtg act gcc atc cgg ttt 686
 Tyr Gly Gly Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe
 190 195 200 205
 ctt ttt ggc ttc ctg ggg ccc ctg gtg gcc gtg gcc agc tgc cac agt 734
 Leu Phe Gly Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser
 210 215 220
 gcc ctc ctg tgc tgg gca gcc cga cgc tgc cgg ccg ctg ggc aca gcc 782
 Ala Leu Leu Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala
 225 230 235
 att gtg gtg ggg ttt ttt gtc tgc tgg gca ccc tac cac ctg ctg ggg 830
 Ile Val Val Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly
 240 245 250
 ctg gtg ctc act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc 878
 Leu Val Leu Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala
 255 260 265
 ctg cgg gct gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc 926
 Leu Arg Ala Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys
 270 275 280 285
 ctc aat ccc atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg 974
 Leu Asn Pro Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg
 290 295 300
 tca ctg cca gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag 1022
 Ser Leu Pro Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln
 305 310 315
 gac gaa agt gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tcg 1070
 Asp Glu Ser Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser
 320 325 330
 gag atg gag gtg tag gctggagaga cattgtgggt gtgtatcttc ttatctcatt 1125
 Glu Met Glu Val
 335
 tcacaagact ggcttcaggc atagctggat ccaggagctc aatgatgtct tcattttatt 1185
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<210> 17
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 17

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Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp

30

Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
260 265 270

- 37 -

Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
 275 280 285

Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
 290 295 300

Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
 305 310 315 320

Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
 325 330 335

Val

<210> 18
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (174)..(1175)

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 tgttttcttt tgtttgtata tatgtttatt ggtaacaggt gacactggaa gca atg 176
 Met
 1
 aac acc aca gtg atg caa ggc ttc aac aga tct gag cgg tgc ccc aga 224
 Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro Arg
 5 10 15
 gac act cgg ata gta cag ctg gta ttc cca gcc ctc tac aca gtg gtt 272
 Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val Val
 20 25 30
 ttc ttg acc ggc atc ctg ctg aat act ttg gct ctg tgg gtg ttt gtt 320
 Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val
 35 40 45
 cac atc ccc agc tcc tcc acc ttc atc atc tac ctc aaa aac act ttg 368
 His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu
 50 55 60 65
 gtg gcc gac ttg ata atg aca ctc atg ctt cct ttc aaa atc ctc tct 416
 Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu Ser
 70 75 80
 gac tca cac ctg gca ccc tgg cag ctc aga gct ttt gtg tgt cgt ttt 464
 Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg Phe

- 38 -

85	90	95	
tct tcg gtg ata ttt tat gag acc atg tat gtg ggc atc gtg ctg tta Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu Leu 100 105 110			512
ggg ctc ata gcc ttt gac aga ttc ctc aag atc atc aga cct ttg aga Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu Arg 115 120 125			560
aat att ttt cta aaa aaa cct gtt ttt gca aaa acg gtc tca atc ttc Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile Phe 130 135 140 145			608
atc tgg ttc ttt ttg ttc ttc atc tcc ctg cca aat acg atc ttg agc Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu Ser 150 155 160			656
aac aag gaa gca aca cca tcg tct gtg aaa aag tgt gct tcc tta aag Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu Lys 165 170 175			704
ggg cct ctg ggg ctg aaa tgg cat caa atg gta aat aac ata tgc cag Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys Gln 180 185 190			752
ttt att ttc tgg act gtt ttt atc cta atg ctt gtg ttt tat gtg gtt Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val Val 195 200 205			800
att gca aaa aaa gta tat gat tct tat aga aag tcc aaa agt aag gac Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys Asp 210 215 220 225			848
aga aaa aac aac aaa aag ctg gaa ggc aaa gta ttt gtt gtc gtg gct Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val Ala 230 235 240			896
gtc ttc ttt gtg tgt ttt gct cca ttt cat ttt gcc aga gtt cca tat Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro Tyr 245 250 255			944
act cac agt caa acc aac aat aag act gac tgt aga ctg caa aat caa Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn Gln 260 265 270			992
ctg ttt att gct aaa gaa aca act ctc ttt ttg gca gca act aac att Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn Ile 275 280 285			1040
tgt atg gat ccc tta ata tac ata ttc tta tgt aaa aaa ttc aca gaa Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr Glu 290 295 300 305			1088
aag cta cca tgt atg caa ggg aga aag acc aca gca tca agc caa gaa Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln Glu 310 315 320			1136
aat cat agc agt cag aca gac aac ata acc tta ggc tga caactgtaca Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly 325 330			1185

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 gattatataa aattttaaatc cacatagatc tattcataag ctgaatgaac cttactaag 1365
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 <212> PRT
 <213> Homo sapiens

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<400> 19

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 20 25 30

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
 35 40 45

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
 50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
 65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
 85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
 100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
 115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
 130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
 145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
 165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
 180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
 195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
 210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
 225 230 235 240

- 41 -

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
325 330

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<212> DNA
<213> Homo sapiens
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atctcttaaa	tatgtggcaa	actat	ttgtc	caaagagatg	tgggtccaaac	ccgtcgaagg	180
ctttataatt	tgggtattaga	taacaaggtg	aacaaaactg	acaataaata	ctccaacgaa		240
ttat	ttttttta	aaataactaag	gggcaaaggc	tattctaagg	ggcaaaacaa	tctattactc	300
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tgttttaaaat	ccggattggc	at	tttttcttt	aataataata	catacaaaaa	ctcagaggggt	420
taataaaagaa	ataattcaaa	gtcctaataa	gtcaacaaac	agatttcatt	ataagctgga		480
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ggcccaggcc	ctgagaatgg	gttcaa	acgg	gccaccacc	ggtaacggta	tcagaaaaa	840
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<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (99) .. (743)
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Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser Ser Pro Pro Asn Ser Val			
200	205	210	
taa tcaagaatac ctccttatga aaataattct gagagcatga atatttgacc			793
ttaaattctcc agtgactcag agcttcaccc acaaactcag gagaacataa gcctgctcgt			853
aaagctcaat ccttctatca tggcaccaat cacaagaacc ttggacgttt gactgactct			913
atccttttctc tcctaactat aaatcctatt tgtgtgtcgt gggatatggaa ggacagatat			973
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agcattataa aaagtgtcaa ataaaaaatt accatcatta tcattaaaat aaattttcac			1273
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acacatgccc tgatatgtaa atgatgattt atgttggcga gtctgagagc aagcccaa			1393
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caaattatct aatctctctg atctatTTTT cctcatctgt aaaatagggtg taataataac			1573
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 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 22

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			20					25					30		

Val	Tyr	His	Pro	Ile	Asn	Gly	Ser	Pro	Asp	Tyr	Gln	Lys	Ala	Lys	Leu
		35					40					45			

Gln	Val	Leu	Gly	Ala	Ile	Gln	Ile	Leu	Asn	Ala	Ala	Met	Ile	Leu	Ala
	50					55					60				

- 44 -

Leu Gly Val Phe Leu Gly Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys
65 70 75 80

His Phe Phe Phe Phe Thr Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala
85 90 95

Val Phe Phe Cys Ser Ser Gly Thr Leu Ser Val Val Ala Gly Ile Lys
100 105 110

Pro Thr Arg Thr Trp Ile Gln Asn Ser Phe Gly Met Asn Ile Ala Ser
115 120 125

Ala Thr Ile Ala Leu Val Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala
130 135 140

Val Asn Ile Gln Ser Leu Arg Ser Cys His Ser Ser Ser Glu Ser Pro
145 150 155 160

Asp Leu Cys Asn Tyr Met Gly Ser Ile Ser Asn Gly Met Val Ser Leu
165 170 175

Leu Leu Ile Leu Thr Leu Leu Glu Leu Cys Val Thr Ile Ser Thr Ile
180 185 190

Ala Met Trp Cys Asn Ala Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser
195 200 205

Ser Pro Pro Asn Ser Val
210

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<212> DNA
<213> Homo sapiens

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<222> (179)..(1276)

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gcacggcaga gagtctggtg ggggtggaggg gctggcctgg cccctctgtc ctgtggaa 178
atg ctg ggg caa gtg gtc acc ctc ata ctc ctc ctg ctc ctc aag gtg 226
Met Leu Gly Gln Val Val Thr Leu Ile Leu Leu Leu Leu Lys Val
1 5 10 15
tat cag ggc aaa gga tgc cag gga tca gct gac cat gtg gtt agc atc 274

- 45 -

Tyr	Gln	Gly	Lys	Gly	Cys	Gln	Gly	Ser	Ala	Asp	His	Val	Val	Ser	Ile		
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tcg	gga	gtg	cct	ctt	cag	tta	caa	cca	aac	agc	ata	cag	acg	aag	gtt	322	
Ser	Gly	Val	Pro	Leu	Gln	Leu	Gln	Pro	Asn	Ser	Ile	Gln	Thr	Lys	Val		
		35					40					45					
gac	agc	att	gca	tgg	aag	aag	ttg	ctg	ccc	tca	caa	aat	gga	ttt	cat	370	
Asp	Ser	Ile	Ala	Trp	Lys	Lys	Leu	Leu	Pro	Ser	Gln	Asn	Gly	Phe	His		
	50					55					60						
cac	ata	ttg	aag	tgg	gag	aat	ggc	tct	ttg	cct	tcc	aat	act	tcc	aat	418	
His	Ile	Leu	Lys	Trp	Glu	Asn	Gly	Ser	Leu	Pro	Ser	Asn	Thr	Ser	Asn		
65					70				75						80		
gat	aga	ttc	agt	ttt	ata	gtc	aag	aac	ttg	agt	ctt	ctc	atc	aag	gca	466	
Asp	Arg	Phe	Ser	Phe	Ile	Val	Lys	Asn	Leu	Ser	Leu	Leu	Ile	Lys	Ala		
			85					90						95			
gct	cag	cag	cag	gac	agt	ggc	ctc	tac	tgc	ctg	gag	gtc	acc	agt	ata	514	
Ala	Gln	Gln	Gln	Asp	Ser	Gly	Leu	Tyr	Cys	Leu	Glu	Val	Thr	Ser	Ile		
			100					105					110				
tct	gga	aaa	gtt	cag	aca	gcc	acg	ttc	cag	gtt	ttt	gta	ttt	gat	aaa	562	
Ser	Gly	Lys	Val	Gln	Thr	Ala	Thr	Phe	Gln	Val	Phe	Val	Phe	Asp	Lys		
		115					120					125					
gtt	gag	aaa	ccc	cgc	cta	cag	ggg	cag	ggg	aag	atc	ctg	gac	aga	ggg	610	
Val	Glu	Lys	Pro	Arg	Leu	Gln	Gly	Gln	Gly	Lys	Ile	Leu	Asp	Arg	Gly		
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aga	tgc	caa	gtg	gct	ctg	tct	tgc	ttg	gtc	tcc	agg	gat	ggc	aat	gtg	658	
Arg	Cys	Gln	Val	Ala	Leu	Ser	Cys	Leu	Val	Ser	Arg	Asp	Gly	Asn	Val		
	145				150					155					160		
tcc	tat	gct	tgg	tac	aga	ggg	agc	aag	ctg	atc	cag	aca	gca	ggg	aac	706	
Ser	Tyr	Ala	Trp	Tyr	Arg	Gly	Ser	Lys	Leu	Ile	Gln	Thr	Ala	Gly	Asn		
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ctc	acc	tac	ctg	gac	gag	gag	gtt	gac	att	aat	ggc	act	cac	aca	tat	754	
Leu	Thr	Tyr	Leu	Asp	Glu	Glu	Val	Asp	Ile	Asn	Gly	Thr	His	Thr	Tyr		
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Thr	Cys	Asn	Val	Ser	Asn	Pro	Val	Ser	Trp	Glu	Ser	His	Thr	Leu	Asn		
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Phe	Leu	Val	Ile	Ile	Val	Ile	Leu	Ser	Ala	Leu	Phe	Leu	Gly	Thr	Leu		
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gcc	tgc	ttc	tgt	gtg	tgg	agg	aga	aag	agg	aag	gag	aag	cag	tca	gag	946	
Ala	Cys	Phe	Cys	Val	Trp	Arg	Arg	Lys	Arg	Lys	Glu	Lys	Gln	Ser	Glu		
			245					250					255				
acc	agt	ccc	aag	gaa	ttt	ttg	aca	att	tac	gaa	gat	gtc	aag	gat	ctg	994	
Thr	Ser	Pro	Lys	Glu	Phe	Leu	Thr	Ile	Tyr	Glu	Asp	Val	Lys	Asp	Leu		
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agc acc atc tac tct atg atc cag tcc cag tct tct gct ccc acg tca	1090
Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser	
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Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys	
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Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile	
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Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg	
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Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val
 35 40 45

Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
 50 55 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
 65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
 85 90 95

Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
 100 105 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
 115 120 125

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
 130 135 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
 145 150 155 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
 165 170 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr
 180 185 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn

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195	200	205
Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro		
210	215	220
Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu		
225	230	235 240
Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu		
	245	250 255
Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu		
	260	265 270
Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly		
	275	280 285
Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser		
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Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys		
305	310	315 320
Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile		
	325	330 335
Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg		
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gggggccccg aggccgcagc ttgcctgcgc gctctgagcc ttcgcaactc gcgagcaaag	180
tttggtggag gcaacgcaa gcctgagtcc tttcttcctc tcgttcccca aatccgaggc	240

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Met Val	
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agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc acc atg gca acc ttg	646
Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala Thr Leu	
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tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag gat acc aca tta gag	694
Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu	
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cca gaa gag cca cca acc aaa tac caa atc tct caa cca gaa gtg tac	742
Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr	
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Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp	
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gcc gcc gtg atc agt tgg act aag gat ggg gtg cac ttg ggg ccc aac	838
Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn	
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aat agg aca gtg ctt att ggg gag tac ttg cag ata aag ggc gcc acg	886
Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr	
85 90 95	
cct aga gac tcc ggc ctc tat gct tgt act gcc agt agg act gta gac	934
Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp	
100 105 110	
agt gaa act tgg tac ttc atg gtg aat gtc aca gat gcc atc tca tcc	982
Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser	
115 120 125 130	
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Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu	
135 140 145	
aac agt aac aac aag aga gca cca tac tgg acc aac aca gaa aag atg	1078
Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met	
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gaa aag cgg ctc cat gct gtg cct gcg gcc aac act gtc aag ttt cgc	1126
Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg	
165 170 175	
tgc cca gcc ggg ggg aac cca atg cca acc atg cgg tgg ctg aaa aac	1174
Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn	
180 185 190	

- 50 -

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aac cag cac tgg agc ctc att atg gaa agt gtg gtc cca tct gac aag Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys 215 220 225	1270
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acg tac cac ctg gat gtt gtg gag cga tcg cct cac cgg ccc atc ctc Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu 245 250 255	1366
caa gcc gga ctg ccg gca aat gcc tcc aca gtg gtc gga gga gac gta Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val 260 265 270	1414
gag ttt gtc tgc aag gtt tac agt gat gcc cag ccc cac atc cag tgg Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp 275 280 285 290	1462
atc aag cac gtg gaa aag aac ggc agt aaa tac ggg ccc gac ggg ctg Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu 295 300 305	1510
ccc tac ctc aag gtt ctc aag cac tcg ggg ata aat agt tcc aat gca Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser Asn Ala 310 315 320	1558
gaa gtg ctg gct ctg ttc aat gtg acc gag gcg gat gct ggg gaa tat Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly Glu Tyr 325 330 335	1606
ata tgt aag gtc tcc aat tat ata ggg cag gcc aac cag tct gcc tgg Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser Ala Trp 340 345 350	1654
ctc act gtc ctg cca aaa cag caa gcg cct gga aga gaa aag gag att Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys Glu Ile 355 360 365 370	1702
aca gct tcc cca gac tac ctg gag ata gcc att tac tgc ata ggg gtc Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val 375 380 385	1750
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ctg acc aaa cgt atc ccc ctg cgg aga cag gta aca gtt tcg gct gag Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu 420 425 430	1894
tcc agc tcc tcc atg aac tcc aac acc ccg ctg gtg agg ata aca aca Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr	1942

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435	440	445	450	
cgc ctc tct tca acg gca gac acc ccc atg ctg gca ggg gtc tcc gag				1990
Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu				
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tat gaa ctt cca gag gac cca aaa tgg gag ttt cca aga gat aag ctg				2038
Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu				
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aca ctg ggc aag ccc ctg gga gaa ggt tgc ttt ggg caa gtg gtc atg				2086
Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met				
	485	490	495	
gcg gaa gca gtg gga att gac aaa gac aag ccc aag gag gcg gtc acc				2134
Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr				
	500	505	510	
gtg gcc gtg aag atg ttg aaa gat gat gcc aca gag aaa gac ctt tct				2182
Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser				
	515	520	525	530
gat ctg gtg tca gag atg gag atg atg aag atg att ggg aaa cac aag				2230
Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys				
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aat atc ata aat ctt ctt gga gcc tgc aca cag gat ggg cct ctc tat				2278
Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr				
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gtc ata gtt gag tat gcc tct aaa ggc aac ctc cga gaa tac ctc cga				2326
Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg				
	565	570	575	
gcc cgg agg cca ccc ggg atg gag tac tcc tat gac att aac cgt gtt				2374
Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val				
	580	585	590	
cct gag gag cag atg acc ttc aag gac ttg gtg tca tgc acc tac cag				2422
Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln				
	595	600	605	610
ctg gcc aga ggc atg gag tac ttg gct tcc caa aaa tgt att cat cga				2470
Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg				
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gat tta gca gcc aga aat gtt ttg gta aca gaa aac aat gtg atg aaa				2518
Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys				
	630	635	640	
ata gca gac ttt gga ctc gcc aga gat atc aac aat ata gac tat tac				2566
Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr				
	645	650	655	
aaa aag acc acc aat ggg cgg ctt cca gtc aag tgg atg gct cca gaa				2614
Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu				
	660	665	670	
gcc ctg ttt gat aga gta tac act cat cag agt gat gtc tgg tcc ttc				2662
Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe				
	675	680	685	690

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ggg att ccc gtg gag gaa ctt ttt aag ctg ctg aag gaa gga cac aga	2758
Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg	
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atg gat aag cca gcc aac tgc acc aac gaa ctg tac atg atg atg agg	2806
Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg	
725 730 735	
gac tgt tgg cat gca gtg ccc tcc cag aga cca acg ttc aag cag ttg	2854
Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu	
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755 760 765 770	
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Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp	
775 780 785	
aca aga agt tct tgt tct tca gga gat gat tct gtt ttt tct cca gac	2998
Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp	
790 795 800	
ccc atg cct tac gaa cca tgc ctt cct cag tat cca cac ata aac ggc	3046
Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly	
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Ser Val Lys Thr	
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Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
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Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
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Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
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Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
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Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
          85             90             95

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Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
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Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
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Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
 145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
 165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
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Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
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Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
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Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
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Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
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His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
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Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
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Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
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Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
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Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
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Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
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Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
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Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
 690 695 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
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Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
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Cys Pro Pro Lys Thr Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly
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Lys Cys Ile Ser Arg Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu
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Phe Glu Phe His Cys Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg
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Cys Ile His Gly Ser Arg Gln Cys Asp Arg Glu Tyr Asp Cys Lys Asp	
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Cys Asn Met Ala Arg Asp Cys Arg Asp Trp Ser Asp Glu Pro Ile Lys	
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Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
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Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
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Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
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Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
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Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
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Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
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Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
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Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
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Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu
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Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp
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Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn
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Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu
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Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
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Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
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Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys
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Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys
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Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln
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Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser
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Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala

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Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys	530	535	540
Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile	545	550	555
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Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile	610	615	620
Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn	625	630	635
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Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu	690	695	700
Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala	705	710	715
			720

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Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
 740 745 750

Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
 755 760 765

His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
 770 775 780

Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
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Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
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Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
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 Met Thr Pro Ile Leu Thr Val Leu Ile
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 Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Val Gln Ala Gly His
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 Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Ile Gln
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 Gly Ser Pro Val Thr Leu Arg Cys Gln Gly Ser Leu Gln Ala Glu Glu
 45 50 55
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 Tyr His Leu Tyr Arg Glu Asn Lys Ser Ala Ser Trp Val Arg Arg Ile
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 Gln Glu Pro Gly Lys Asn Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp
 75 80 85
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 Glu His Ala Gly Arg Tyr His Cys Gln Tyr Tyr Ser His Asn His Ser
 90 95 100 105
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 Ser Glu Tyr Ser Asp Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ser
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 aaa ccc acc ctc tca gct ctg ccc agc cct gtg gtg acc tta gga ggg 498
 Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val Val Thr Leu Gly Gly
 125 130 135
 aac gtg acc ctc cag tgt gtc tca cag gtg gca ttt gac ggc ttc att 546
 Asn Val Thr Leu Gln Cys Val Ser Gln Val Ala Phe Asp Gly Phe Ile
 140 145 150
 ctg tgt aag gaa gga gaa gat gaa cac cca caa cgc ctg aac tcc cat 594
 Leu Cys Lys Glu Gly Glu Asp Glu His Pro Gln Arg Leu Asn Ser His
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 Ser Pro Tyr Val Trp Ser Leu Pro Ser Asp Leu Leu Glu Leu Leu Val
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 Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Met
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 35 40 45

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
 50 55 60

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
 65 70 75 80

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
 85 90 95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
 100 105 110

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
 115 120 125

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
 130 135 140

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
 145 150 155 160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
 165 170 175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
 180 185 190

- 70 -

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
 195 200 205

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
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Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
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Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
 245 250 255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
 260 265 270

Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
 275 280 285

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
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Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
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Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
 325 330 335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
 340 345 350

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
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Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
 370 375 380

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
 385 390 395 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
 405 410 415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
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Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile

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435

440

445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

Gly Arg
465